RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/602,475*

Source: *I Fw o*

Date Processed by STIC: *11/6/03*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: /0/602,475

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____Wrapped Nucleics
   Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____Misaligned Amino
   Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____PatentIn 2.0
   "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____Skipped Sequences
   (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____Skipped Sequences
   (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____Use of n's or Xaa's
   (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____Invalid <213>
    Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____PatentIn 2.0
    "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____Misuse of n/Xaa
"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 11/06/2003
PATENT APPLICATION: **US/10/602,475**   TIME: 09:57:13

Input Set : **A:\UF-325XC1.txt**
Output Set: **N:\CRF4\11062003\J602475.raw**

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   3 <110> APPLICANT: Klee, Harry J.
   4        Lashbrook, Coralie
   5        Shrode, Lori
   7 <120> TITLE OF INVENTION: Materials and Methods for Tissue-Specific Targeting of
Ethylene
   8        Insensitivity in Transgenic Plants
  10 <130> FILE REFERENCE: UF-325XC1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/602,475
C--> 12 <141> CURRENT FILING DATE: 2003-06-23
  12 <150> PRIOR APPLICATION NUMBER: US 60/390,385
  13 <151> PRIOR FILING DATE: 2002-06-21
  15 <160> NUMBER OF SEQ ID NOS: 4
  17 <170> SOFTWARE: PatentIn version 3.2
  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 773
  21 <212> TYPE: PRT
  22 <213> ORGANISM: Amino acid sequence alignment of ETR2
  24 <400> SEQUENCE: 1
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  27 1               5                   10                  15
  30 Phe Val Ser Pro Val Leu Ala Ile Asn Gly Gly Gly Tyr Pro Arg Cys
  31             20                  25                  30
  34 Asn Cys Glu Asp Glu Gly Asn Ser Phe Trp Ser Thr Glu Asn Ile Leu
  35         35                  40                  45
  38 Glu Thr Gln Arg Val Ser Asp Phe Leu Ile Ala Val Ala Tyr Phe Ser
  39       50                  55                  60
  42 Ile Pro Ile Glu Leu Leu Tyr Phe Val Ser Cys Ser Asn Val Pro Phe
  43 65                  70                  75                  80
  46 Lys Trp Val Leu Phe Glu Phe Ile Ala Phe Ile Val Leu Cys Gly Met
  47             85                  90                  95
  50 Thr His Leu Leu His Gly Trp Thr Tyr Ser Ala His Pro Phe Arg Leu
  51             100                 105                 110
  54 Met Met Ala Phe Thr Val Phe Lys Met Leu Thr Ala Leu Val Ser Cys
  55         115                 120                 125
  58 Ala Thr Ala Ile Thr Leu Ile Thr Leu Ile Pro Leu Leu Leu Lys Val
  59       130                 135                 140
  62 Lys Val Arg Glu Phe Met Leu Lys Lys Lys Ala His Glu Leu Gly Arg
  63 145                 150                 155                 160
  66 Glu Val Gly Leu Ile Leu Ile Lys Lys Glu Thr Gly Phe His Val Arg
  67             165                 170                 175
  70 Met Leu Thr Gln Glu Ile Arg Lys Ser Leu Asp Arg His Thr Ile Leu
  71         180                 185                 190
  74 Tyr Thr Thr Leu Val Glu Leu Ser Lys Thr Leu Gly Leu Gln Asn Cys
  75         195                 200                 205
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Input Set : **A:\UF-325XC1.txt**
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 79     210             215                 220
 82 Glu Leu Arg Gly Arg Gly Gly Tyr Gly Gly Cys Ser Val Ser Met Glu
 83 225             230                 235                 240
 86 Asp Leu Asp Val Val Arg Ile Arg Glu Ser Asp Glu Val Asn Val Leu
 87             245                 250                 255
 90 Ser Val Asp Ser Ser Ile Ala Arg Ala Ser Gly Gly Gly Gly Asp Val
 91             260                 265                 270
 94 Ser Glu Ile Gly Ala Val Ala Ala Ile Arg Met Pro Met Leu Arg Val
 95         275                 280                 285
 98 Ser Asp Phe Asn Gly Glu Leu Ser Tyr Ala Ile Leu Val Cys Val Leu
 99     290                 295                 300
102 Pro Gly Gly Thr Pro Arg Asp Trp Thr Tyr Gln Glu Ile Glu Ile Val
103 305             310                 315                 320
106 Lys Val Val Ala Asp Gln Val Thr Val Ala Leu Asp His Ala Ala Val
107             325                 330                 335
110 Leu Glu Glu Ser Gln Leu Met Arg Glu Lys Leu Ala Glu Gln Asn Arg
111             340                 345                 350
114 Ala Leu Gln Met Ala Lys Arg Asp Ala Leu Arg Ala Ser Gln Ala Arg
115         355                 360                 365
118 Asn Ala Phe Gln Lys Thr Met Ser Glu Gly Met Arg Arg Pro Met His
119     370                 375                 380
122 Ser Ile Leu Gly Leu Leu Ser Met Ile Gln Asp Glu Lys Leu Ser Asp
123 385             390                 395                 400
126 Glu Gln Lys Met Ile Val Asp Thr Met Val Lys Thr Gly Asn Val Met
127             405                 410                 415
130 Ser Asn Leu Val Gly Asp Ser Met Asp Val Pro Asp Gly Arg Phe Gly
131             420                 425                 430
134 Thr Glu Met Lys Pro Phe Ser Leu His Arg Thr Ile His Glu Ala Ala
135         435                 440                 445
138 Cys Met Ala Arg Cys Leu Cys Leu Cys Asn Gly Ile Arg Phe Leu Val
139         450                 455                 460
142 Asp Ala Glu Lys Ser Leu Pro Asp Asn Val Val Gly Asp Glu Arg Arg
143 465             470                 475                 480
146 Val Phe Gln Val Ile Leu His Ile Val Gly Ser Leu Val Lys Pro Arg
147             485                 490                 495
150 Lys Arg Gln Glu Gly Ser Ser Leu Met Phe Lys Val Leu Lys Glu Arg
151         500                 505                 510
154 Gly Ser Leu Asp Arg Ser Asp His Arg Trp Ala Ala Trp Arg Ser Pro
155         515                 520                 525
158 Ala Ser Ser Ala Asp Gly Asp Val Tyr Ile Arg Phe Glu Met Asn Val
159     530                 535                 540
162 Glu Asn Asp Asp Ser Ser Ser Gln Ser Phe Ala Ser Val Ser Ser Arg
163 545             550                 555                 560
166 Asp Gln Glu Val Gly Asp Val Arg Phe Ser Gly Gly Tyr Gly Leu Gly
167             565                 570                 575
170 Gln Asp Leu Ser Phe Gly Val Cys Lys Lys Val Val Gln Leu Ile His
171         580                 585                 590
174 Gly Asn Ile Ser Val Val Pro Gly Ser Asp Gly Ser Pro Glu Thr Met
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PATENT APPLICATION: **US/10/602,475**   TIME: 09:57:13

Input Set : **A:\UF-325XC1.txt**
Output Set: **N:\CRF4\11062003\J602475.raw**

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175         595                600                605
178 Ser Leu Leu Leu Arg Phe Arg Arg Arg Pro Ser Ile Ser Val His Gly
179     610                615                620
182 Ser Ser Glu Ser Pro Ala Pro Asp His His Ala His Pro His Ser Asn
183 625                630                635                640
186 Ser Leu Leu Arg Gly Leu Gln Val Leu Leu Val Asp Thr Asn Asp Ser
187             645                650                655
190 Asn Arg Ala Val Thr Arg Lys Leu Leu Glu Lys Leu Gly Cys Asp Val
191         660                665                670
194 Thr Ala Val Ser Ser Gly Phe Asp Cys Leu Thr Ala Ile Ala Pro Gly
195         675                680                685
198 Ser Ser Ser Pro Ser Thr Ser Phe Gln Val Val Val Leu Asp Leu Gln
199     690                695                700
202 Met Ala Glu Met Asp Gly Tyr Glu Val Ala Met Arg Ile Arg Ser Arg
203 705                710                715                720
206 Ser Trp Pro Leu Ile Val Ala Thr Thr Val Ser Leu Asp Glu Glu Met
207             725                730                735
210 Trp Asp Lys Cys Ala Gln Ile Gly Ile Asn Gly Val Val Arg Lys Pro
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214 Val Val Leu Arg Ala Met Glu Ser Glu Leu Arg Arg Val Leu Leu Gln
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225 <213> ORGANISM: Amino acid sequence alignment of ETR2
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232 tcagatttgt ctctatctct tcactttaa gtcttctggt tttgtcatca ccagcttttt     180
234 ttgttctgtc tctgtctttc tctttgtgta tttttattct cgtcatcgtt gttcttctat    240
236 gagaggaaga tcggaatgtc gaagagaatt agaagattct cgtacatcac ttcgttggaa    300
238 tttcacaggt cgatgagaga tctgagaact gtttcatttt gatccaaact catctctttc    360
240 agagtataat ggactaagca tttttttct ccgaagatgg ttaaagaaat agcttcttgg      420
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244 tatccacgat gtaactgcga agacgaagga aacagtttct ggagtacaga gaacattcta    540
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248 ttactttact tcgtgagttg ttccaatgtt ccattcaaat gggttctctt tgagtttatc    660
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252 ccatttagat taatgatggc gtttactgtt ttcaagatgt tgactgcttt agtctcttgt    780
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256 tttatgctta agaagaaagc tcatgagctt ggtcgtgaag ttggtttgat tttgattaag    900
258 aaagagactg gctttcatgt tcgtatgctt actcaagaga ttcgtaagtc tttggatcgt    960
260 catacgattc tttatactac tttggttgag ctttcgaaga ctttagggtt gcagaattgt   1020
262 gcggtttgga tgccgaatga cggtggaacg gagatggatt tgactcatga gttgagaggg   1080
264 agaggtggtt atggtggttg ttctgtttct atggaggatt tggatgttgt taggattagg   1140
266 gagagtgatg aagtgaatgt gttgagtgtt gactcgtcca ttgctcgagc tagtggtggt   1200
268 ggtggggatg ttagtgagat tggtgccgtg gctgctatta gaatgccgat gcttcgtgtt   1260
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270 tcggatttta atggagagct aagttatgcg atacttgttt gtgttttacc gggcgggacg  1320
272 cctcgggatt ggacttatca ggagattgag attgttaaag ttgtggcgga tcaagtaacc  1380
274 gttgcgttag atcatgcagc ggttcttgaa gagtctcagc ttatgaggga gaagctggcg  1440
276 gaacagaaca gggcgttgca gatggcgaag agagacgcgt tgagagcgag ccaagcgagg  1500
278 aatgcgtttc agaaaacgat gagcgaaggg atgaggcgtc ctatgcattc gatactcggt  1560
280 cttttgtcga tgattcagga cgagaagttg agtgacgagc agaaaatgat tgttgatacg  1620
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288 tctctacctg ataatgtagt aggtgatgaa agaagggtct ttcaagtgat acttcatata  1860
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292 ttgaaagaaa gaggaagctt ggataggagt gatcatagat gggctgcttg gagatcaccg  1980
294 gcttcttcag cagatggaga tgtgtatata agatttgaaa tgaatgtaga gaatgatgat  2040
296 tcaagttctc aatcatttgc ttctgtttcc tccagagatc aagaagttgg tgatgttaga  2100
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300 cagttgattc atgggaatat ctcggtggtc cctggctcgg atggttcacc ggagaccatg  2220
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308 gggtgcgatg taaccgcggt ttcctctgga ttcgattgcc ttaccgccat tgctcccggc  2460
310 tcgtcctcgc cttctacttc gtttcaagtg gtggtgcttg atcttcaaat ggcagagatg  2520
312 gacggttatg aagtggccat gaggatcagg agtcgatctt ggccgttgat tgtggcgacg  2580
314 acagtgagct tggatgaaga aatgtgggac aagtgtgcac agattggaat caatggagtt  2640
316 gtgagaaagc cagtggtgtt aagagctatg gagagtgagc tccgaagagt attgttgcaa  2700
318 gctgaccaac ttctctaagt tgttatctca acttctcttc tacattcaaa atttttacac  2760
320 catagattta tgtcaaatat atcaaaatga aatttcgaaa ttgttattat atataccacc  2820
322 catatctcta tgatttgtac atcctgtttt tttttgttct ttttctcatt ttgaacccca  2880
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340 1               5                   10                  15
342 tta atg aaa tac caa tac atc tcc gat ttc ttc att gcg att gcg tat   96
343 Leu Met Lys Tyr Gln Tyr Ile Ser Asp Phe Phe Ile Ala Ile Ala Tyr
344             20                  25                  30
346 ttt tcg att cct ctt gag ttg att tac ttt gtg aag aaa tca gcc gtg  144
347 Phe Ser Ile Pro Leu Glu Leu Ile Tyr Phe Val Lys Lys Ser Ala Val
348         35                  40                  45
350 ttt ccg tat aga tgg gta ctt gtt cag ttt ggt gct ttt atc gtt ctt  192
351 Phe Pro Tyr Arg Trp Val Leu Val Gln Phe Gly Ala Phe Ile Val Leu
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356 65              70              75              80
358 aga acc gtg gcg ctt gtg atg act acc gcg aag gtg tta acc gct gtt      288
359 Arg Thr Val Ala Leu Val Met Thr Thr Ala Lys Val Leu Thr Ala Val
360             85              90              95
362 gtc tcg tgt gct act gcg ttg atg ctt gtt cat att att cct gat ctt      336
363 Val Ser Cys Ala Thr Ala Leu Met Leu Val His Ile Ile Pro Asp Leu
364             100             105             110
366 ttg agt gtt aag act cgg gag ctt ttc ttg aaa aat aaa gct gct gag      384
367 Leu Ser Val Lys Thr Arg Glu Leu Phe Leu Lys Asn Lys Ala Ala Glu
368             115             120             125
370 ctc gat aga gaa atg gga ttg att cga act cag gaa gaa acc gga agg      432
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374 cat gtg aga atg ttg act cat gag att aga agc act tta gat aga cat      480
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376 145             150             155             160
378 act att tta aag act aca ctt gtt gag ctt ggt agg aca tta gct ttg      528
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380             165             170             175
382 gag gag tgt gca ttg tgg atg cct act aga act ggg tta gag cta cag      576
383 Glu Glu Cys Ala Leu Trp Met Pro Thr Arg Thr Gly Leu Glu Leu Gln
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386 ctt tct tat aca ctt cgt cat caa cat ccc gtg gag tat acg gtt cct      624
387 Leu Ser Tyr Thr Leu Arg His Gln His Pro Val Glu Tyr Thr Val Pro
388             195             200             205
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392     210             215             220
394 aaa ata tct cct aat tct cct gtg gct agg ttg aga cct gtt tct ggg      720
395 Lys Ile Ser Pro Asn Ser Pro Val Ala Arg Leu Arg Pro Val Ser Gly
396 225             230             235             240
398 aaa tat atg cta ggg gag gtg gtc gct gtg agg gtt ccg ctt ctc cac      768
399 Lys Tyr Met Leu Gly Glu Val Val Ala Val Arg Val Pro Leu Leu His
400             245             250             255
402 ctt tct aat ttt cag att aat gac tgg cct gag ctt tca aca aag aga      816
403 Leu Ser Asn Phe Gln Ile Asn Asp Trp Pro Glu Leu Ser Thr Lys Arg
404             260             265             270
406 tat gct ttg atg gtt ttg atg ctt cct tca gat agt gca agg caa tgg      864
407 Tyr Ala Leu Met Val Leu Met Leu Pro Ser Asp Ser Ala Arg Gln Trp
408             275             280             285
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412     290             295             300
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415 Val Ala Leu Ser His Ala Ala Ile Leu Glu Glu Ser Met Arg Ala Arg
416 305             310             315             320
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419 Asp Leu Leu Met Glu Gln Asn Val Ala Leu Asp Leu Ala Arg Arg Glu
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VERIFICATION SUMMARY   DATE: 11/06/2003
PATENT APPLICATION: **US/10/602,475**   TIME: 09:57:14

Input Set : **A:\UF-325XC1.txt**
Output Set: **N:\CRF4\11062003\J602475.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date